

AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning at page 4, line 31, as follows:

Figure 7 : Tandem mass spectroscopy fragmentation pattern of the acid hydrolysate produced from Mtp samples (A), actual identifications are indicated in red (bold) and theoretically possible fragments are black (B) (SEQ ID NO: 1).

Please amend the paragraph beginning at page 15, line 12, as follows:

Upon examination of the LC-MS/MS results, it was found that all three samples analyzed had one common peptide fragment having a monoisotopic mass (Mr) of 1086.55 Da and a sequence of PGAAPPPPAAGGGA (SEQ ID NO: 1) (aa101-114) (Figure 7A). Mascot uses a probability based score and in all cases, the identification of the the fragment 101-114 was considered statistically significant, indicating a true identification. Furthermore, two of the samples produced only this peptide following acid hydrolysis indicating the relative purity of the analytes. Obtaining identical results using three different digested Mtp samples strongly suggests that the identified fragment (Figure 7) represents a portion of the Mtp structural subunit, the MtpA pilin.

Please delete the originally filed Sequence Listing.

Page 48 (Abstract), after the last line, beginning on a new page, please insert the attached Substitute Sequence Listing.